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10/607,706	06/27/2003	Paul O. Sheppard	97-04D3	4538

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CHRISTINE BELLAS
AMGEN
1201 AMGEN COURT WEST
SEATTLE, WA 98119-3105

EXAMINER	
ROMEO, DAVID S	
ART UNIT	PAPER NUMBER
1647	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	01/24/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	10/607,706	SHEPPARD ET AL.	
	Examiner	Art Unit	
	David S. Romeo	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *01 November 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-22* is/are pending in the application.

4a) Of the above claim(s) *4-6,10-12,16-18 and 20-22* is/are withdrawn from consideration.

5)☒ Claim(s) *19* is/are allowed.

6)☒ Claim(s) *1-3,7-9 and 13-15* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1-22* are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *1106*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Claims 1–22 are pending.

Applicant's election of group I, claims 1–3, 7–9 and 13–15 in the reply filed on 11/01/2006 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Claims 4–6, 10–12, 16–18 and 20–22 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on 11/01/2006.

Claims 1–3, 7–9, 13–15 and 19 are being examined.

Claim Rejections - 35 USC § 112

Claims 1–3, 7–9 and 13–15 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide molecule encoding an isolated peptide, wherein the peptide is selected from the group consisting of: a) residues 2 to 18 of SEQ ID NO:11; b) residues 2 to 14 of SEQ ID NO:11; c) residues 3 to 18 of SEQ ID NO:11; d) residues 3 to 14 of SEQ ID NO:11; e) residues 4 to 18 of SEQ ID NO:11; f) residues 4 to 14 of SEQ ID NO:11; g) residues 1 to 11 of SEQ ID NO:11; h) residues 1 to 10 of SEQ ID NO:11; and i) residues 2 to 11 of SEQ ID NO:11, does not reasonably provide enablement for an isolated polynucleotide molecule encoding an isolated peptide molecule as shown in SEQ ID NO:12, said peptide molecule consisting of residues X through Y, wherein X is an integer from 1 to 4, inclusive, and wherein Y is 14 or 18, and wherein at least (Y minus X) minus 2 residues are as in the corresponding region of SEQ ID NO:11 (claim 1); an isolated polynucleotide molecule

according to claim 1, wherein at least (Y minus X) minus 1 residues are as in the corresponding region of SEQ ID NO:11 (claim 2); an isolated polynucleotide molecule according to claim 2, wherein at least (Y minus X) residues are as in the corresponding region of SEQ ID NO:11; an isolated polynucleotide molecule encoding an isolated peptide molecule as shown in SEQ ID NO:12, said peptide molecule consisting of residues X through 11, wherein X is 1 or 2, and wherein at least (11 minus X) minus 2 residues are as in the corresponding region of SEQ ID NO:11 (claim 7); an isolated polynucleotide molecule according to claim 7, wherein at least (11 minus X) minus 1 residues are as in the corresponding region of SEQ ID NO:11 (claim 8); an isolated polynucleotide molecule according to claim 9, wherein at least 11 minus X residues are as in the corresponding region of SEQ ID NO:11 (claim 9); an isolated polynucleotide molecule encoding an isolated peptide molecule as shown in SEQ ID NO:12, said peptide molecule consisting of residues 1 through 10, and wherein at least seven residues are as in the corresponding region of SEQ ID NO:11 (claim 13); an isolated polynucleotide according to claim 13, wherein at least eight residues are as in the corresponding region of SEQ ID NO:11; (claim 14); an isolated polynucleotide according to claim 13, wherein at least nine are as in the corresponding region of SEQ ID NO:11 (claim 15). The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

The claims are directed to or encompass the genus of all polynucleotides that vary due to the degeneracy of the genetic code encoding the genus of all the variant polypeptides. The only apparent use of the claimed degenerate polynucleotides is in the production of the encoded polypeptides. Therefore, it is appropriate to consider enablement of the claimed genus of

polynucleotides in terms of enablement of the encoded genus of polypeptides. There are no functional limitations to polypeptides. Thus, the claims encompass the genus of all polynucleotides that vary due to the degeneracy of the genetic code encoding the genus of all the variant polypeptides, wherein the polypeptides possess any and/or all possible functions or activities.

The specification discloses the following:

> The novel peptide fragments (shown in SEQ ID NO:11) have been designated Truncated Motilin-Like (TML) peptides and are also shown in Table A. Variants of this fragment are also described herein and shown in SEQ ID NO:12. Thus, residues 1 through 18 of SEQ ID NOs:11 and 12 correspond to residues 24 to 41 of SEQ ID NO:2. SEQ ID NO: 10 shows the polynucleotide sequence encoding SEQ ID NO:11. Page 6, last full paragraph.
>
> The active TML peptides are predicted to result from a C-terminal cleavage after amino acid residue 37 (Gln) or residue 41 (Ser) of SEQ ID NO: 2. ... Therefore, a peptide based on cleavage after amino acid 37 of SEQ ID NO: 2 (Gln) was synthesized and resulted in a 14 amino acid peptide with biological activity (from amino acid residue 24 (Gly) to amino acid residue 37 (Gln) of SEQ ID NO: 2). Page 7, full paragraph 3.
>
> Multiple signal peptidase cleavages are expected in the present invention. Thus, the amino terminal of the TML peptides may begin with glycine, residue 1 of SEQ ID NO:11, serine, residues 2 or 3 of SEQ ID NO:11 or phenylalanine, residue 4 of SEQ ID NO:11. Page 7, full paragraph 4.
>
> Based on analysis of the motilin family, residues 4 to 9 of SEQ ID NO:11 will be essential for receptor binding and activation. (Miller, P. et al., Peptides 16(1):11-18, 1995; and Peeters, T. L. et al,. Peptides 13(6):1103-1107, 1992). It should be noted that serine (residue 29 of SEQ ID NO:4) has been shown to be an isoleucine by Schubert, H. et al., Can. J. Biochem. 52:7-8, 1974. Furthermore, this analysis suggests that residues 4 (Phe), 5 (Leu), 6 (Ser) and 9 (His) of SEQ ID NO:11 are particularly important residues for receptor binding and/or activity.

However, there are no working examples of receptor binding and/or activity of peptides with less than amino acid residue 24 (Gly) to amino acid residue 37 (Gln) of SEQ ID NO: 2. Nor are they any working examples of receptor binding and/or activity of peptides with less than 100%

identity to amino acid residue 24 (Gly) to amino acid residue 37 (Gln) of SEQ ID NO: 2. The examiner is aware working examples are not required. Lack of a working example is, however, a factor to be considered. The specification also lacks guidance for making and working examples of polypeptides possessing any and/or all possible functions or activities. Some of the variants do not even comprise the residues that the specification hypothesizes will be essential for receptor binding and activation. Furthermore, Hosoda (J Biol Chem. 2003 Jan 3;278(1):64-70) teaches that *n*-octanoyl modification of Ser^3 is essential of ghrelin's function (page 64, right column, full paragraph 1). Moreover, there is a lack of predictability in the art. Predicting structure, hence function, from primary amino acid sequence data is extremely complex and there doesn't exist an efficient algorithm for predicting the structure of a given protein from its amino acid sequence alone. See Bowie (Science, (1990 Mar 16) 247 (4948) 1306-10) page 1306, column 1, full paragraph 1, or Ngo (The Protein Folding Problem and Tertiary Structure Prediction, Merz and Le Grand (Eds), August 1994, Springer Verlag, pages 433 and 492-495) page 433, full paragraph 1, and page 492, full paragraph 2. A practitioner would have to resort to a substantial amount of undue, random, trial and error experimentation wherein the variants peptides are made and tested for a useful activity. The current claim scope is analogous to that of claim 7 of U.S. Patent No. 4,703,008, which was held to be invalid under 35 U.S.C. § 112, first paragraph, for want of enablement in Amgen Inc. v. Chugai Pharmaceuticals Co. Ltd., 18 USPQ 2d, 1016 (CAFC, 3/5/91, see page 1026, section D). In that instance a claim to a nucleic acid molecule encoding a polypeptide having an amino acid sequence sufficiently duplicative of the amino acid sequence of erythropoietin (EPO) so as to have a specified biological activity was held to be invalid under 35 U.S.C. § 112, first paragraph, for want of enablement. The disclosure

upon which that claim was based described a recombinant DNA encoding EPO and a few analogs thereof. That disclosure differs from the present specification because, whereas the present specification describes single working example of a DNA encoding residue 24 (Gly) to amino acid residue 37 (Gln) of SEQ ID NO: 2, it does not describe even a single working example of a variant thereof. The court held that what is necessary to support claims of this breadth is a disclosure sufficient to enable one skilled in the art to carry out the invention commensurate with the scope of the claims. For DNA sequences, that means disclosing how to make and use enough sequences to justify the grant of the patent protection sought in the present claims. The present specification is even more limited than the '008 patent because it describes only a single protein and no analogs or mutants thereof and, therefore, provides even less support than the '008 specification for claims of comparable scope and which were held to be invalid in that patent.

To practice the present invention in a manner consistent with the breadth of the claims would not require just a repetition of work that is described in the present application but a substantial inventive contribution on the part of a practitioner which would involve the determination of all possible functions or activities of the encoded genus of peptides. It is this additional characterization of that single disclosed, naturally occurring protein that constitutes undue experimentation.

In view of the breadth of the claims, the limited amount of direction and working examples provided by the inventor, the unpredictability in the art and the quantity of experimentation needed to make or use the invention based on the content of the disclosure, it

would require undue experimentation for the skilled artisan to use the full scope of the claimed invention.

Claims 1–3, 7–9 and 13–15 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are directed to or encompass the genus of all polynucleotides that vary due to the degeneracy of the genetic code encoding the genus of all the variant polypeptides. The only apparent use of the claimed degenerate polynucleotides is in the production of the encoded polypeptides. Therefore, it is appropriate to consider description of the claimed genus of polynucleotides in terms of description of the encoded genus of polypeptides. There are no functional limitations to polypeptides. Thus, the claims encompass the genus of all polynucleotides that vary due to the degeneracy of the genetic code encoding the genus of all the variant polypeptides, wherein the polypeptides possess any and/or all possible functions or activities.

Vas-Cath Inc. v. Mahurkar , 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written description' inquiry, whatever is now claimed." (See page 1117). The specification does not "clearly allow persons

of ordinary skill in the art to recognize that [he or she] invented what is claimed." (see Vas-Cath at page 1116).

With the exception of residue 24 (Gly) to amino acid residue 37 (Gln) of SEQ ID NO: 2, the skilled artisan cannot envision the detailed chemical structure of the encompassed peptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993) and Amgen Inc v. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016.

One cannot describe what one has not conceived. See Fiddes v. Baird, 30 USPQ2d 1481, 1483. In Fiddes v. Baird, claims directed to mammalian FGFs were found unpatentable due to lack of written description for the broad class. The specification provided only the bovine sequence.

Therefore, only residue 24 (Gly) to amino acid residue 37 (Gln) of SEQ ID NO: 2 but not the full breadth of the claim meets the written description provision of 35 U.S.C. 112, first paragraph. Applicant is reminded that Vas-Cath Inc. v. Mahurkar , 19 USPQ2d 1111makes clear that the written description provision of 35 USC 112 is severable from its enablement provision. (See page 1115).

Claim 9 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 9 is a dependent claim that depends from itself, and thus makes no sense. The metes and bounds are not clearly set forth.

Claims 1–3, 7–9 and 13–15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The claims are directed to or encompass an isolated polynucleotide encoding an isolated peptide consisting of residues X through Y of SEQ ID NO: 12, wherein "at least" 7 to 17 residues are as in the corresponding region of SEQ ID NO: 11. The peptide is 10 to 18 amino acids long. A peptide consisting of 10 to 18 residues cannot comprise "at least" any given number of amino acid residues because: firstly, the transitional phrase "consisting of" limits only residues X through Y of SEQ ID NO: 12 and excludes any number of residues greater than 10 to 18; secondly, the phrase "at least" has no upper limit and reads on residues outside the "residues X through Y" range and outside the 7 to 17 residues range. The metes and bounds are not clearly set forth.

For examination purposes the following is how the examiner construes the claims:

a polynucleotide encoding a peptide consisting of residues 4 to 14 of SEQ ID NO: 12, wherein at least 8 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 3 to 14 of SEQ ID NO: 12, wherein at least 9 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 14 of SEQ ID NO: 12, wherein at least 10 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 14 of SEQ ID NO: 12, wherein at least 11 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 4 to 18 of SEQ ID NO: 12, wherein at least 12 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 3 to 18 of SEQ ID NO: 12, wherein at least 13 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 18 of SEQ ID NO: 12, wherein at least 14 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 18 of SEQ ID NO: 12, wherein at least 15 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 4 to 14 of SEQ ID NO: 12, wherein at least 9 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 3 to 14 of SEQ ID NO: 12, wherein at least 10 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 14 of SEQ ID NO: 12, wherein at least 11 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 14 of SEQ ID NO: 12, wherein at least 12 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 4 to 18 of SEQ ID NO: 12, wherein at least 13 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 3 to 18 of SEQ ID NO: 12, wherein at least 14 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 18 of SEQ ID NO: 12, wherein at least 15 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 18 of SEQ ID NO: 12, wherein at least 16 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 4 to 14 of SEQ ID NO: 12, wherein at least 10 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 3 to 14 of SEQ ID NO: 12, wherein at least 11 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 14 of SEQ ID NO: 12, wherein at least 12 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 14 of SEQ ID NO: 12, wherein at least 13 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 4 to 18 of SEQ ID NO: 12, wherein at least 14 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 3 to 18 of SEQ ID NO: 12, wherein at least 15 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 18 of SEQ ID NO: 12, wherein at least 16 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 18 of SEQ ID NO: 12, wherein at least 17 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 11 of SEQ ID NO: 12, wherein at least 7 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 11 of SEQ ID NO: 12, wherein at least 8 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 11 of SEQ ID NO: 12, wherein at least 8 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 11 of SEQ ID NO: 12, wherein at least 9 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 2 to 11 of SEQ ID NO: 12, wherein at least 9 residues are as in the corresponding region of SEQ ID NO: 11;

a polynucleotide encoding a peptide consisting of residues 1 to 11 of SEQ ID NO: 12, wherein at least 10 residues are as in the corresponding region of SEQ ID NO: 11;

peptide consisting of residues 1 to 10 of SEQ ID NO: 12, wherein at least 7 residues are as in the corresponding region of SEQ ID NO: 11;

peptide consisting of residues 1 to 10 of SEQ ID NO: 12, wherein at least 8 residues are as in the corresponding region of SEQ ID NO: 11;

peptide consisting of residues 1 to 10 of SEQ ID NO: 12, wherein at least 9 residues are as in the corresponding region of SEQ ID NO: 11.

The interpretation of the claims does not relieve applicants from responding to the instant rejection.

Double Patenting

Claims 1–3, 7–9 and 13–15 rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1–16 of U.S. Patent No. 6,939,690. Although the conflicting claims are not identical, they are not patentably distinct from each other

because each set of claims is directed to encompasses a polynucleotide encoding residue 24 (Gly) to amino acid residue 37 (Gln) or amino acid 41 (Ser) of SEQ ID NO: 2.

Conclusion

Claim 19 is allowable.

ANY INQUIRY CONCERNING THIS COMMUNICATION OR EARLIER COMMUNICATIONS FROM THE EXAMINER SHOULD BE DIRECTED TO DAVID S. ROMEO WHOSE TELEPHONE NUMBER IS (571) 272-0890. THE EXAMINER CAN NORMALLY BE REACHED ON MONDAY THROUGH FRIDAY FROM 9:00 A.M. TO 5:30 P.M. IF ATTEMPTS TO REACH THE EXAMINER BY TELEPHONE ARE UNSUCCESSFUL, THE EXAMINER'S SUPERVISOR, BRENDA BRUMBACK, CAN BE REACHED ON (571) 272-0961.

IF SUBMITTING OFFICIAL CORRESPONDENCE BY FAX, APPLICANTS ARE ENCOURAGED TO SUBMIT OFFICIAL CORRESPONDENCE TO THE CENTRAL FAX NUMBER FOR OFFICIAL CORRESPONDENCE, WHICH IS (571) 273-8300.

CUSTOMERS ARE ALSO ADVISED TO USE CERTIFICATE OF FACSIMILE PROCEDURES WHEN SUBMITTING A REPLY TO A NON-FINAL OR FINAL OFFICE ACTION BY FACSIMILE (SEE 37 CFR 1.6 AND 1.8).

ANY INQUIRY OF A GENERAL NATURE OR RELATING TO THE STATUS OF THIS APPLICATION OR PROCEEDING MAY BE OBTAINED FROM THE PATENT APPLICATION INFORMATION RETRIEVAL (PAIR) SYSTEM. STATUS INFORMATION FOR PUBLISHED APPLICATIONS MAY BE OBTAINED FROM EITHER PRIVATE PAIR OR PUBLIC PAIR. STATUS INFORMATION FOR UNPUBLISHED APPLICATIONS IS AVAILABLE THROUGH PRIVATE PAIR ONLY. FOR MORE INFORMATION ABOUT THE PAIR SYSTEM, SEE HTTP://PAIR-DIRECT.USPTO.GOV. CONTACT THE ELECTRONIC BUSINESS CENTER (EBC) AT 866-217-9197 (TOLL-FREE) FOR QUESTIONS ON ACCESS TO THE PRIVATE PAIR SYSTEM,

DAVID ROMEO
PRIMARY EXAMINER
ART UNIT 1647

DSR
JANUARY 22, 2007